



APPENDIX
IN THE SPECIFICATION

Please amend the following paragraph beginning at page 9, line 34 and ending at page 10, line 11, to read as follows:

Present databases and computers allow rapid searches for partners based on surrogate sequences. Examples of available computer based programs to analyse sequences include BLAST, Patternfind, ExPASy, MEME (Multiple EM for Motif Elicitation), [<http://meme.sdsc.edu/meme/website/intro.html>], (<http://meme.sdsc.edu/meme/website/intro.html>), MAST (Motif Alignment and Search Tool, <http://meme.sdsc.edu/mem/website/mast-intro.html>). [(www.expasy.ch/) and] (www.expasy.ch/) and ISREC (www.isrec.isb-sib.ch/software/software.html) [www.isrec.isb-sib.ch/software/software.html] Identification of surrogates provides tools for partner identification, phenotyping and small molecule discovery. Given that a site directed assay is available at this early stage for the unknown target, high throughout screening allows the rapid identification of reactive small molecules of low target affinity. Combinatorial chemistry, allows for improvements in potency which would then provide small molecules for phenotyping and testing in animal models.

Please amend the following paragraph beginning at page 19, line 34 to page 20, line 3, to read as follows:

Sequencing of randomly selected clones from the cell library indicated that about 54% of all clones were in-frame. The short FLAG sequence DYKD(SEQ ID NO: 1), was included at

the N-terminus as an immunoaffinity tag. In addition, the E-tag epitope (GAPVPYPDPLEPR) (SEQ ID NO: 2) was engineered into the carboxy terminus of the peptide.

Please amend the following paragraph beginning at page 21, line 27, to read as follows:

The panning experiments identified a surrogate peptide, KcB7, with the amino acid sequence RKEMGGGGPGWSENLFQ(SEQ ID NO: 3). A Blastp search, using several different queries revealed TNFR1 which is the natural biological partner of TNF β .

Please amend the following section, beginning at page 21, line 34 to page 22, line 28, to read as follows:

BLASTp search results for the TNF β Surrogate peptide KcB7

Query: WSENLFQ(SEQ ID NO: 4)

Database: nr

Sequences producing significant alignments:	Score (bits)	E Value
prf 2102238A tumor necrosis factor alpha inhibitor [Homo s...	20	2419
gb AAA36756.1 (M60275) TNF receptor [Homo sapiens]	20	2419
pdb 1TNR R Chain R, Tumor Necrosis Factor Receptor P55 ...	20	2419
pdb 1NCF A Chain A, Binding Protein, Cytokine Mol_id: 1; Mo...	20	2419
ref NP_001056.1 tumor necrosis factor receptor 1 (55kD) >g...	20	2419

>prf|2102238A tumor necrosis factor alpha inhibitor [Homo sapiens]
Length = 160

Score = 20.4 bits (41), Expect = 2419
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 1 WSENLFQ 7(SEQ ID NO: 4)

WSENLFQ
Sbjct: 96 WSENLFQ 102(SEQ ID NO: 4)

>gb|AAA36756.1| (M60275) TNF receptor [Homo sapiens]
Length = 453

Score = 20.4 bits (41), Expect = 2419
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 1 WSENLFQ 7(SEQ ID NO: 4)
WSENLFQ
Sbjct: 136 WSENLFQ 142(SEQ ID NO: 4)

>pdb|1TNR|R Chain R, Tumor Necrosis Factor Receptor P55 (Extracellular
Domain) Complexed With Tumor Necrosis Factor-Beta
Length = 139

Score = 20.4 bits (41), Expect = 2419
Identities = 7/7 (100%), Positives = 7/7 (100%)

Please amend the following paragraph beginning at page 22, line 31 to page 23, line 8, to
read as follows:

Patternfind search results for the TNF-β Surrogate peptide KcB7

Query sequence: WSENLFQ (SEQ ID NO: 4)

II. DATABASE: NONREDUNDANT

Limit 10

gp|M60275|339760|AC886035F969E231 TNF receptor [Homo sapiens]
Occurrences: 1
Position : 136 WSENLFQ(SEQ ID NO: 4)

sp|P19438|TNR1_HUMAN|4CEFBA96D03B8225 (TNFRSF1A..)TUMOR NECROSIS
FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN
1) (TBPI) (P60) (TNF-R1) (TNF-RI) (P55) (CD120A).[Homo sapiens]
Occurrences: 1
Position : 136 WSENLFQ(SEQ ID NO: 4)

2 matches found

Please amend the following paragraph beginning at page 23, line 10, to read as follows:

Closer examination of the complementary sequences revealed that the short N-terminal sequence RKEMG(Piece Of SEQ ID NO: 3)and the C-terminal sequence WSENLFQ (SEQ ID NO: 4) were identical to regions on TNFR1 (amino acids 77-81 and 107-113 respectively). These segments corresponded to amino acids within two critical ligand:receptor contact domains. In the case of the N-terminal grouping, the surrogate contained 5 of the 15 amino acids of the 77-81 contact domain whereas in the C-terminal grouping, the surrogate contained 6 of the 9 amino acids identified within the 107-113 contact domain.

Please amend the following section, beginning at page 23, line 20 to page 24, line 5, to read as follows:

Comparison with human TNFR1 extracellular domain

IYPSGVIGLVPHLGDRKRDSCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTD
CRECesgsFTASENHLRhc*LscSkC***RkeMg**QVEISSCTVDRDTVCGRKNQYRHYWSENLF
qcFNCSLCLNGTVHLSCQEKKQNTVCTCHAGFFLRENECVSCS(SEQ ID NO: 5)

Contact residues are based on Banner et al., (1993) Cell 73: 431-445.

Bold= contacted by TNF β subunit A

lower case = contacted by TNF β subunit C

italics = contacted by TNF β both subunits A and C

Underline = homology to the ϕ clone

TNF β

LPGVGLTPSAAQTARQHPKMHLAHLSTLKPAAHLIGDPSK**Q**NSLLWR**R**ANTDRAFLQDGFSLSNNSSLVPTSGIYFVYSQVFSG**K**A YSPKAPSSpLyLAHEVQLFSsqypfHvPLLSSqKmVYPGL**Q**EPWLHSMYHGAAFQLTQGDQLSThTd**G**IPHLVLSPSTVFFGAFAL(SEQ ID NO: 6)

Bold = TNF β subunit A

lower case = TNF β subunit C

Please amend the following section, beginning at page 24, line 8, to read as follows:

Comparison with human TNFR2 extracellular domain

rKEMGGGGGGpgwSENIFQ(SEQ ID NO: 7)

LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSYTQLWNWVPECLSCGSRCSSDQVETQACTrEQNRICTrpgwYCAISKQEGCRLCAPRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASRDAVCTSTSPT(SEQ ID NO: 8)

Please amend the following section beginning at page 26, line 20, to read as follows:

HCV ALIGNMENTS

eIF3: EDLDNIQTPE-SVLLSAVSGEDTQDRT**D**RLLLTPWVKFLWESY(SEQ ID NO: 10)

CONSENSUS **T**x**R**LL(SEQ ID NO: 11)

HCV-NG-D9 **T**SGESSG**D**RTR**R**VL**T**SSSARTLPN(SEQ ID NO: 12)

HCV-3-F5 **I**VTGQP--SQLLGGAVCGP-**S**TP**R**LRTGLCRLSGT(SEQ ID NO: 13)

HCV-3-H8 RRTCGDPAAMLERL**S**CRAVDYRGASHT**G**RLLNLRGMHQYP(SEQ ID NO: 14)

HCV-3-C3 FTT**P**R**H**LSGRT**V**OMMRDSTS(SEQ ID NO: 15)

Please amend the following section beginning at page 26, line 26, to read as follows:

**OUTPUT FROM ADVANCED BLAST SEARCH FOR HCV mRNA SURROGATE
QUERY - SEARCH 1:**

Query sequence: TSGESSGDRTRRVLT(SEQ ID NO: 16)
Program: blastp
Database: swissprot
Expect value: 10000

Please amend the following section, beginning at page 26, line 33 to page 28, line 35, to read as follows:

OUTPUT:

		Sequences producing significant alignments:	Score	E	Value
				(bits)	
sp P31258 HXAB_CHICK	HOMEobox protein HOX-A11 (GHOX-1I) (CH...).		20	477	
sp P23116 IF3A_MOUSE	EUKARYOTIC TRANSLATION INITIATION FACT...		19	1072	
sp P39690 KHS1_YEAST	KILLER TOXIN KHS PRECURSOR (KILLER OF ...)		19	1072	
sp O83264 NUSG_TREPA	TRANSCRIPTION ANTITERMINATION PROTEIN ...		19	1072	
sp P13079 CARB_STRTH	RRNA METHYLTRANSFERASE (CARBOMYCIN-RES...).		19	1072	
sp Q14152 IF3A_HUMAN	EUKARYOTIC TRANSLATION INITIATION FACT...		19	1072	
sp P39925 AFG3_YEAST	MITOCHONDRIAL RESPIRATORY CHAIN COMPLE...		19	1072	
sp P16561 HEMA_VACCT	HEMAGGLUTININ PRECURSOR		19	1404	
sp P52023 DP3B_SYNPT	DNA POLYMERASE III, BETA CHAIN		19	1404	
sp P20978 HEMA_VACCC	HEMAGGLUTININ PRECURSOR		19	1404	
sp P15989 CA36_CHICK	COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR		19	1404	

List truncated here...

>sp|P31258|HXAB_CHICK HOMEobox protein HOX-A11 (GHOX-1I) (CHOX-1.9)

Length = 297

Score = 20.4 bits (41), Expect = 477
Identities = 8/11 (72%), Positives = 9/11 (81%)

Query: 2 SGESSGDRTRR 12 (SEQ ID NO: 17)

SG SSG RTR+

Sbjct: 217 SGSSSGQRTRK 227 (SEQ ID NO: 18)

>sp|P23116|IF3A_MOUSE EUKARYOTIC TRANSLATION INITIATION FACTOR 3
SUBUNIT 10 (EIF-3 THETA)
(EIF3 P167) (EIF3 P180) (EIF3 P185) (P162 PROTEIN)
(CENTROSOMIN)
Length = 1344

Score = 19.2 bits (38), Expect = 1072
Identities = 8/13 (61%), Positives = 10/13 (76%)

Query: 2 SGESSGDRTRRVL 14(SEQ ID NO: 19)

SGE + DRT R+L

Sbjct: 133 SGEDTQDRTDRL 145(SEQ ID NO: 20)

>sp|P39690|KHS1_YEAST KILLER TOXIN KHS PRECURSOR (KILLER OF HEAT
SENSITIVE)
Length = 708

Score = 19.2 bits (38), Expect = 1072
Identities = 8/13 (61%), Positives = 10/13 (76%)

Query: 3 GESSGDRTRRVLT 15(SEQ ID NO: 21)

G+SSG T+R LT

Sbjct: 98 GKSSGSATKRGLT 110(SEQ ID NO: 22)

>sp|O83264|NUSG_TREPA TRANSCRIPTION ANTITERMINATION PROTEIN NUSG
Length = 185

Score = 19.2 bits (38), Expect = 1072
Identities = 7/12 (58%), Positives = 9/12 (74%)

Query: 2 SGESSGDRTRRV 13(SEQ ID NO: 23)

+GE GDRT R+

Sbjct: 117 AGEIKGDRTPRI 128(SEQ ID NO: 24)

>sp|P13079|CARB_STRTH RRNA METHYLTRANSFERASE (CARBOMYCIN-
RESISTANCE PROTEIN)
Length = 299

Score = 19.2 bits (38), Expect = 1072
Identities = 8/12 (66%), Positives = 8/12 (66%)

Query: 2 SGESSGDRTRRV 13(SEQ ID NO: 23)

SG S DR RRV
Sbjct: 40 SGRSEADRRRRV 51(SEQ ID NO: 25)

>sp|Q14152|IF3A_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3
SUBUNIT 10 (EIF-3 THETA)
(EIF3 P167) (EIF3 P180) (EIF3 P185) (KIAA0139)
Length = 1382

Score = 19.2 bits (38), Expect = 1072
Identities = 8/13 (61%), Positives = 10/13 (76%)

Query: 2 SGESSGDRTRRVL 14(SEQ ID NO: 19)
SGE + DRT R+L
Sbjct: 133 SGEDTQDRTDRLL 145(SEQ ID NO: 26)

>sp|P39925|AFG3_YEAST MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES
ASSEMBLY PROTEIN AFG3
(TAT-BINDING HOMOLOG 10)
Length = 761

Score = 19.2 bits (38), Expect = 1072
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 2 SGESSGDRTRRVLT 15(SEQ ID NO: 27)
S +SGD + RVLT
Sbjct: 136 SSNNSGDDSNRVLT 149(SEQ ID NO: 28)

Please amend the following section beginning at page 29, line 1 to page 32, line 30, to read as follows:

OUTPUT FROM ADVANCED BLAST SEARCH FOR HCV mRNA

SURROGATE QUERY - SEARCH 2:

Query sequence: TSGESSGDRTRRVLTSSS(SEQ ID NO: 29)

Program: blastp

Database: swissprot

Expect value: -e 10000

Sequences producing significant alignments:	Score E (bits)	Value
sp Q01728 NAC1_RAT SODIUM/CALCIUM EXCHANGER 1 PRECURSOR (NA... sp P70414 NAC1_MOUSE SODIUM/CALCIUM EXCHANGER 1 PRECURSOR (... sp P48765 NAC1_BOVIN SODIUM/CALCIUM EXCHANGER 1 PRECURSOR (...	21 21 20	65 65 190

sp P48766 NAC1_CAVPO	SODIUM/CALCIUM EXCHANGER 1 PRECURSOR (...)	20	190
sp P32418 NAC1_HUMAN	SODIUM/CALCIUM EXCHANGER 1 PRECURSOR (...)	20	190
sp P23685 NAC1_CANFA	SODIUM/CALCIUM EXCHANGER 1 PRECURSOR (...)	20	190
sp P48767 NAC1_FELCA	SODIUM/CALCIUM EXCHANGER 1 PRECURSOR (...)	20	190
sp P08173 ACM4_HUMAN	MUSCARINIC ACETYLCHOLINE RECEPTOR M4	19	249
sp P23116 IF3A_MOUSE	EUKARYOTIC TRANSLATION INITIATION FACT...	19	249
sp Q14152 IF3A_HUMAN	EUKARYOTIC TRANSLATION INITIATION FACT...	19	249
sp P15656 FGF5_MOUSE	FIBROBLAST GROWTH FACTOR-5 PRECURSOR (...)	19	327
sp P30042 ES1_HUMAN	ES1 PROTEIN HOMOLOG PRECURSOR (PROTEIN ...)	19	327
sp O35491 CLK2_MOUSE	PROTEIN KINASE CLK2	18	428
sp P49760 CLK2_HUMAN	PROTEIN KINASE CLK2	18	428
sp P15172 MYOD_HUMAN	MYOBlast DETERMINATION PROTEIN 1 (MYOG...)	18	428
sp O75069 Y481_HUMAN	HYPOTHETICAL PROTEIN KIAA0481 (HH1480)	18	428
sp P02533 K1CN_HUMAN	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOK...	18	561
sp P30989 NTR1_HUMAN	NEUROTENSIN RECEPTOR TYPE 1 (NT-R-1) (...)	18	561
sp P30551 CCKR_RAT	CHOLECYSTOKININ TYPE A RECEPTOR (CCK-A R...	18	561
sp Q08369 GATA4_MOUSE	TRANSCRIPTION FACTOR GATA-4 (GATA BIND...	18	561

List truncated here...

>sp|Q01728|NAC1_RAT SODIUM/CALCIUM EXCHANGER 1 PRECURSOR
(NA+/CA2+-EXCHANGE PROTEIN 1)
Length = 971

Score = 21.2 bits (43), Expect = 65
Identities = 9/15 (60%), Positives = 11/15 (73%)

Query: 3 GE~~SSGDRTRRVLTSS~~ 17(SEQ ID NO: 30)
GE G RT ++LTSS
Sbjct: 933 GELGGPRTAKLLTSS 947(SEQ ID NO: 31)

>sp|P70414|NAC1_MOUSE SODIUM/CALCIUM EXCHANGER 1 PRECURSOR
(NA+/CA2+-EXCHANGE PROTEIN 1)
Length = 970

Score = 21.2 bits (43), Expect = 65
Identities = 9/15 (60%), Positives = 11/15 (73%)

Query: 3 GE~~SSGDRTRRVLTSS~~ 17(SEQ ID NO: 30)
GE G RT ++LTSS
Sbjct: 932 GELGGPRTAKLLTSS 946(SEQ ID NO: 32)

>sp|P48765|NAC1_BOVIN SODIUM/CALCIUM EXCHANGER 1 PRECURSOR
(NA+/CA2+-EXCHANGE PROTEIN 1)
Length = 970

Score = 19.6 bits (39), Expect = 190
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 3 GESSGDRTRRVLTS 16(SEQ ID NO: 33)
GE G RT ++LTS
Sbjct: 932 GELGGPRTAKLLTS 945(SEQ ID NO: 34)

>sp|P48766|NAC1_CAVPO SODIUM/CALCIUM EXCHANGER 1 PRECURSOR
(NA+/CA2+-EXCHANGE PROTEIN 1)
Length = 970

Score = 19.6 bits (39), Expect = 190
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 3 GESSGDRTRRVLTS 16(SEQ ID NO: 33)
GE G RT ++LTS
Sbjct: 932 GELGGPRTAKLLTS 945(SEQ ID NO: 35)

>sp|P32418|NAC1_HUMAN SODIUM/CALCIUM EXCHANGER 1 PRECURSOR
(NA+/CA2+-EXCHANGE PROTEIN 1)
Length = 970

Score = 19.6 bits (39), Expect = 190
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 3 GESSGDRTRRVLTS 16(SEQ ID NO: 33)
GE G RT ++LTS
Sbjct: 932 GELGGPRTAKLLTS 945(SEQ ID NO: 36)

>sp|P23685|NAC1_CANFA SODIUM/CALCIUM EXCHANGER 1 PRECURSOR
(NA+/CA2+-EXCHANGE PROTEIN 1)
Length = 970

Score = 19.6 bits (39), Expect = 190
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 3 GESSGDRTRRVLTS 16(SEQ ID NO: 33)
GE G RT ++LTS
Sbjct: 932 GELGGPRTAKLLTS 945(SEQ ID NO: 37)

>sp|P48767|NAC1_FELCA SODIUM/CALCIUM EXCHANGER 1 PRECURSOR
(NA+/CA2+-EXCHANGE PROTEIN 1)

Length = 970

Score = 19.6 bits (39), Expect = 190
Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 3 GESSGDRTRRVLTS 16(SEQ ID NO: 33)

GE G RT ++LTS

Sbjct: 932 GELGGPRTAKLLTS 945(SEQ ID NO: 38)

>sp|P08173|ACM4_HUMAN MUSCARINIC ACETYLCHOLINE RECEPTOR M4
Length = 479

Score = 19.2 bits (38), Expect = 249
Identities = 8/14 (57%), Positives = 13/14 (92%)

Query: 5 SSGDRTRRVLTSSS 18(SEQ ID NO: 39)

SSG+++ R++TSSS

Sbjct: 10 SSGNQSVRLVTSSS 23(SEQ ID NO: 40)

>sp|P23116|IF3A_MOUSE EUKARYOTIC TRANSLATION INITIATION FACTOR 3
SUBUNIT 10 (EIF-3 THETA)
(EIF3 P167) (EIF3 P180) (EIF3 P185) (P162 PROTEIN)
(CENTROSOMIN)
Length = 1344

Score = 19.2 bits (38), Expect = 249
Identities = 8/13 (61%), Positives = 10/13 (76%)

Query: 2 SGESSGDRTRRVL 14(SEQ ID NO: 19)

SGE + DRT R+L

Sbjct: 133 SGEDTQDRTDRLL 145(SEQ ID NO: 20)

>sp|Q14152|IF3A_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3
SUBUNIT 10 (EIF-3 THETA)
(EIF3 P167) (EIF3 P180) (EIF3 P185) (KIAA0139)
Length = 1382

Score = 19.2 bits (38), Expect = 249
Identities = 8/13 (61%), Positives = 10/13 (76%)

Query: 2 SGESSGDRTRRVL 14(SEQ ID NO: 19)

SGE + DRT R+L

Sbjct: 133 SGEDTQDRTDRLL 145(SEQ ID NO: 26)

>sp|P15656|FGF5_MOUSE FIBROBLAST GROWTH FACTOR-5 PRECURSOR (FGF-5) (HBGF-5)
Length = 264

Score = 18.8 bits (37), Expect = 327
Identities = 9/16 (56%), Positives = 10/16 (62%)

Query: 3 GESSGDRTRRVLTSSS 18(SEQ ID NO: 41)

G+SSG R R T SS

Sbjct: 39 GDSSGSRGRSSATFSS 54(SEQ ID NO: 42)

>sp|P30042|ES1_HUMAN ES1 PROTEIN HOMOLOG PRECURSOR (PROTEIN KNP-I) (GT335)
Length = 268

Score = 18.8 bits (37), Expect = 327
Identities = 8/18 (44%), Positives = 11/18 (60%)

Query: 1 TSGESSGDRTRRVLTSSS 18(SEQ ID NO: 43)

T G+ S +R VLT S+

Sbjct: 93 TKGQPSEGESRNVLTESA 110(SEQ ID NO: 44)

>sp|O35491|CLK2_MOUSE PROTEIN KINASE CLK2
Length = 499

Score = 18.4 bits (36), Expect = 428
Identities = 8/11 (72%), Positives = 8/11 (72%)

Query: 2 SGESSGDRTRR 12(SEQ ID NO: 17)

S SS DRTTRR

Sbjct: 34 SWSSSSDRTRR 44(SEQ ID NO: 45)

>sp|P49760|CLK2_HUMAN PROTEIN KINASE CLK2
Length = 499

Score = 18.4 bits (36), Expect = 428
Identities = 8/11 (72%), Positives = 8/11 (72%)

Query: 2 SGESSGDRTRR 12(SEQ ID NO: 17)

S SS DRTTRR

Sbjct: 34 SWSSSSDRTRR 44(SEQ ID NO: 46)

Please amend the following section beginning at page 33, line 3, to read as follows:

Output from Patternfind for HCV mRNA surrogate query

Query sequence: DRTxRLL(SEQ ID NO: 47)
Database: Nonredundant
Limit: 10

sp|Q14152|IF3A_HUMAN|485C01B28D67EBBA (EIF3S10)EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3 THETA) (EIF3 P167) (EIF3 P180) (EIF3 P185) (KIAA0139).[Homo sapiens]
Occurrences: 1
Position : 139 DRTDRLL(SEQ ID NO: 48)

sp|P4637 3|FAS1_RHOFA|A66B6F3DF1286566 (FAS1..)CYTOCHROME P450 FAS1 (EC 1.14.--).[Rhodococcus fascians]

Occurrences: 1
Position : 170 DRTARLL(SEQ ID NO: 49)

sp|P23116|IF3A_MOUSE|F4CAE2169F577712 (EIF3S10..)EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3 THETA) (EIF3 P167) (EIF3 P180) (EIF3 P185) (P162 PROTEIN) (CENTROSOMIN).[Mus musculus]
Occurrences: 1

Position : 139 DRTDRLL(SEQ ID NO: 50)

Please amend the following paragraph, beginning at page 34, line 15, to read as follows:

In addition, several peptides from each pan showed the presence of the **RGG** box, a well-defined RNA-binding motif, as indicated below. RGG sequences in each surrogate is in bold and underlined. (SEQ ID NOS 51-65, respectively, in order of appearance)

M1 - 3 - B7	RGLFTEWFR <u>RGG</u> SWSNYRVTS
M1 - 3 - E8	TDGGRSVISDNVR <u>RGG</u> SRLWLWIRHGSWSQAWGPQDAWSSK
M1 - 3 - H6	RVSSAQPGCTSRRFRC <u>RGG</u> LLFNGVTSTNPKTGLSNAQ
M1 - 4 - H1	VVYVGVLSYWPHLSGGGRL <u>RGG</u> FGC <u>RGG</u>
M2 - 3 - C1	WPPGRTLSDL <u>RGG</u> GAGARGM
M2 - 3 - C9	SSGGHLRWSAL <u>RGG</u> HGHGLA
M2 - 3 - E2	AMRLKPIAFKGPRAGAGWVEV <u>RGG</u> FAACT <u>RGG</u> SHHH
M2 - 3 - E3	LHAGWDVTAPRACKGA <u>RGG</u> QGPGLHGRFYCH <u>RGG</u> LCGLGRC
M2 - 3 - E9	DE <u>RGG</u> SLKGKLRGALVRLGMGHAMP <u>RGG</u> VWPSTGRPSKQG
M2 - 3 - H12	WTPRHGPMPRCWRHQ <u>RGG</u> SVFPVGAGPHWALWPIK <u>RGG</u> RTA
M2 - NG - C7	RKTGSNIWLPLYHKVCPASTRAGN <u>RGG</u> SRFLWGSMQTNC
M3 - 3 - B9	RLQR <u>RGG</u> AVAVVWVGFVGVL <u>RGG</u> WGRLLLIIILGWVLMWF
M3 - 3 - C2	QHSEHGGTEWRK <u>RGG</u> MAFAASFLCMRDSYRTTRLRSLLG
M3 - 3 - C7	GTRHVINVRDSSGVPCRKFGGLQFSQMGKCTIP <u>RGG</u> A
M4 - NG - A4	VL <u>RGG</u> SVGKGSLMWQCEDWRTGGPRSNLWGLWNGR <u>RGG</u> PK

Please amend the following paragraph beginning at page 34, line 32 to page 35, line 4, to read as follows:

Furthermore, one sequence was found from panning the 20-mer random peptide library on target M1 that contained the KH motif, which is also a known RNA-binding motifs. The surrogate motif corresponding to the KH domain is in bold and underlined.

KH Motif **VIGxxGxxF** (SEQ ID NO: 66)
M1 - 3 - C6 **GV**I**GG**R**GLLF**P**SGFL**H**QHR** (SEQ ID NO: 67)

Please amend the following paragraph beginning at page 37, line 1, to read as follows:

Sequences of Peptide Binders to Tie-1(SEQ ID NOS 68-72, respectively, in order of appearance)

Consensus :	GxAVVFLDRWGNP
>RPT13	SLWGCSGRAVLFLDSVGNPTGTVRC
>RPT9	RRVDAGGAVVYLDRWGNVSV
>RPT34	VVFLDRWGNPQYLGVKASGG
TI1-G11-R40	GPFSWLFETEWGNPKTVPGADRNHRHGRWDPGPVSDYGT

Please amend the following paragraph beginning at page 38, line 33 to page 39, line 2 to read as follows:

The complete ORF of the Tie-1 gene is cloned from fetal human brain (Clontech Quick-Clone cDNA) or fetal human heart using the following primers:

5' Tie-1 forward: GGT CGG CCT CTG GAG TAT GGT CTG(SEQ ID NO: 76)
3' Tie-1 reverse: TCC TTG AGG CAG CTT AAG TCA GAG(SEQ ID NO: 77)

Please amend the following paragraph beginning at page 39, line 3, to read as follows:

The complete ORF of the EGFR gene is cloned from the above libraries or from a placental cDNA library (Clontech Placenta Marathon ready cDNA) using the following primers:

5' EGFR forward: GGA GCA GCG ATG CGA CCC TC(SEQ ID NO: 78)
3' EGFR reverse: GGT CCT GGG TAT CGA AAG AGT CTG G(SEQ ID NO:

79)

Please amend the following paragraph, beginning at page 39, line 10, to read as follows:

In the chimeric receptor, the extracellular and transmembrane regions of Tie-1 are joined to the cytoplasmic kinase domain of the EGFR with an NHE I site which will add the amino acids alanine and serine at the junction. The primers for generating the chimeric receptor are the following primers (with the NHE site underlined):

EGFR forward: GCG CTG CTA GCC GAA GGC GCC ACA TCG TTC(SEQ ID NO: 80)

Tie-1 reverse: GCT GCT GCT AGC GAT GCA CAC CAG GGT TAA AAG G
(SEQ ID NO: 81)